



Exhibit C

BLAST Analysis of SEQ ID NO:1

BLASTN 1.2.3-Paracel [2001-11-20]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Database: gsnMouse; humRNA

129,541 sequences; 199,339,278 total letters

Query= LEX413bestorf
(1116 letters)

| Sequences producing significant alignments: | Score (bits) | E Value |
|--|-----------------|------------|
| BC029118 ACCESSION:BC029118 NID:20809627 Homo sapiens Homo sa... | <u>2212</u> | 0.0 |
| AJ308569 ACCESSION:AJ308569 NID:14330408 Homo sapiens Homo sa... | <u>2204</u> | 0.0 |
| AK057808 ACCESSION:AK057808 NID:16553760 Homo sapiens Homo sa... | <u>2196</u> | 0.0 |
| AK021919 ACCESSION:AK021919 NID:10433216 Homo sapiens Homo sa... | <u>256</u> | 2e-66 |

>BC029118 ACCESSION:BC029118 NID:20809627 Homo sapiens Homo sapiens,
leucine-rich repeat-containing 2, clone MGC:34065
IMAGE:5183639, mRNA, complete cds. humRNA
Length = 1946

Score = 2212 bits (1116), Expect = 0.0
Identities = 1116/1116 (100%)
Strand = Plus / Plus

```
Query: 1      atgggacataaaagtgggtgtcttcgacatttctgtcatcagagccttggtgggaaactcgt 60
              |||
Sbjct: 166    atgggacataaaagtgggtgtcttcgacatttctgtcatcagagccttggtgggaaactcgt 225

Query: 61      gtcaagaagcacaaagcttggcagaagaaggaggtggaaaggcttgagaagagcgccttg 120
              |||
Sbjct: 226    gtcaagaagcacaaagcttggcagaagaaggaggtggaaaggcttgagaagagcgccttg 285

Query: 121     gagaagataaaggaggaggtggaactttgtggccgaatgcaggaggaagggcatccccag 180
              |||
Sbjct: 286    gagaagataaaggaggaggtggaactttgtggccgaatgcaggaggaagggcatccccag 345

Query: 181     gctgtatactgcaagaatggcttcatacacaccagcgtgcggttcttgacaagattgaa 240
              |||
Sbjct: 346    gctgtatactgcaagaatggcttcatacacaccagcgtgcggttcttgacaagattgaa 405

Query: 241     aggaacactctcacaaaggcagagttcacttcccaaggacagaggcaaacggagcagtgcg 300
```

Sbjct: 406 |||||
 aggaacactctcacaaggcagagttcacttcccaaggacagaggcaaacggagcagtgcg 465

Query: 301 tttgtgtttgaactttctggggagcactggacggagctcccagattcattgaaggagcag 360
 Sbjct: 466 tttgtgtttgaactttctggggagcactggacggagctcccagattcattgaaggagcag 525

Query: 361 acacacctgagagaatggtacataagcaataccttgattcaaatacttctacatatatt 420
 Sbjct: 526 acacacctgagagaatggtacataagcaataccttgattcaaatacttctacatatatt 585

Query: 421 cagttatttcaagcgatgagaattctggatctgcaaaaaaccaaatactcacatcttcca 480
 Sbjct: 586 cagttatttcaagcgatgagaattctggatctgcaaaaaaccaaatactcacatcttcca 645

Query: 481 gcagaaatcgggtgtttgaagaacctgaaagaactcaatgtgggtttcaactatctgaag 540
 Sbjct: 646 gcagaaatcgggtgtttgaagaacctgaaagaactcaatgtgggtttcaactatctgaag 705

Query: 541 agcattcctccagaattgggagattgtgaaaatctagagagactggattgttctggaaat 600
 Sbjct: 706 agcattcctccagaattgggagattgtgaaaatctagagagactggattgttctggaaat 765

Query: 601 ctagaattaatggagctgccctttgaattaagtaatttgaagcaagttacattttagat 660
 Sbjct: 766 ctagaattaatggagctgccctttgaattaagtaatttgaagcaagttacattttagat 825

Query: 661 atctcagcaaacaagttttccagtggtcccaatctgtgtcctgcggatgtcgaatttgcag 720
 Sbjct: 826 atctcagcaaacaagttttccagtggtcccaatctgtgtcctgcggatgtcgaatttgcag 885

Query: 721 tggttggatatcagcagcaataacctgaccgacctgccgcaagatatagacaggctagag 780
 Sbjct: 886 tggttggatatcagcagcaataacctgaccgacctgccgcaagatatagacaggctagag 945

Query: 781 gagctgcagagctttctcttgataaaaaacaagttgacctaccttcctattccatgctg 840
 Sbjct: 946 gagctgcagagctttctcttgataaaaaacaagttgacctaccttcctattccatgctg 1005

Query: 841 aacctgaagaagctcactctgttagtcgtcagtggggaccatttggtggagctcccaact 900
 Sbjct: 1006 aacctgaagaagctcactctgttagtcgtcagtggggaccatttggtggagctcccaact 1065

Query: 901 gccctttgtgactcatccacacctttaaaatttgtaagccttatggacaatcctattgat 960
 Sbjct: 1066 gccctttgtgactcatccacacctttaaaatttgtaagccttatggacaatcctattgat 1125

Query: 961 aatgcccaatgtgaagatggcaatgaaataatggaaagtgaacgggatcgccaacatttt 1020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1126 aatgcccaatgtgaagatggcaatgaaataatggaaagtgaacgggatcgccaacatttt 1185

Query: 1021 gataaagaagttatgaaagcctatatattgaagaccttaaagaaagagaatctgttcccagc 1080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1186 gataaagaagttatgaaagcctatatattgaagaccttaaagaaagagaatctgttcccagc 1245

Query: 1081 tataaccaccaaagtgtcttttagccttcaactttga 1116
 ||||||||||||||||||||||||||||||||
 Sbjct: 1246 tataaccaccaaagtgtcttttagccttcaactttga 1281

>AJ308569 ACCESSION:AJ308569 NID:14330408 Homo sapiens Homo sapiens
 mRNA for leucine-rich repeat-containing 2 protein (LRRC2
 gene). humRNA
 Length = 4860

Score = 2204 bits (1112), Expect = 0.0
 Identities = 1115/1116 (99%)
 Strand = Plus / Plus

Query: 1 atgggacataaagtgggtgtcttcgacatttctgtcatcagagccttgtgggaaactcgt 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 168 atgggacataaagtgggtgtcttcgacatttctgtcatcagagccttgtgggaaactcgt 227

Query: 61 gtcaagaagcacaaagccttggcagaagaaggaggtggaaaggcttgagaagagcgccttg 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 228 gtcaagaagcacaaagccttggcagaagaaggaggtggaaaggcttgagaagagcgccttg 287

Query: 121 gagaagataaaggaggagtggaaactttgtggccgaatgcaggaggaagggcatccccag 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 288 gagaagataaaggaggagtggaaactttgtggccgaatgcaggaggaagggcatccccag 347

Query: 181 gctgtatactgcaagaatggcttcatagacaccagcgtgcggttctggacaagattgaa 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 348 gctgtatactgcaagaatggcttcatagacaccagcgtgcggttctggacaagattgaa 407

Query: 241 aggaacactctcacaaggcagagttcacttccaaggacagaggcaaacggagcagtgcg 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 408 aggaacactctcacaaggcagagttcacttccaaggacagaggcaaacggagcagtgcg 467

Query: 301 tttgtgtttgaactttctggggagcactggacggagctcccagattcattgaaggagcag 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 468 tttgtgtttgaactttctggggagcactggacggagctcccagattcattgaaggagcag 527

Query: 361 acacacctgagagaatggtacataagcaataccttgattcaaatcattcctacatatatt 420
 |||||
 Sbjct: 528 acacacctgagagaatggtacataagcaataccttgattcaaatcattcctacatatatt 587

Query: 421 cagttatttcaagcgatgagaattctggatctgccaaaaaaccaatctcacatcttcca 480
 |||||
 Sbjct: 588 cagttatttcaagcgatgagaattctggatctgccaaaaaaccaatctcacatcttcca 647

Query: 481 gcagaaatcggttggttgaagaacctgaaagaactcaatgtgggtttcaactatctgaag 540
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 Sbjct: 648 gcagaaatcggttggttgaagaacctgaaagaactcaatgtgggtttcaactatctgaag 707

Query: 541 agcattcctccagaattgggagattgtgaaaatctagagagactggattgttctggaaat 600
 |||||
 Sbjct: 708 agcattcctccagaattgggagattgtgaaaatctagagagactggattgttctggaaat 767

Query: 601 ctagaattaatggagctgccctttgaattaagtaatttgaagcaagttacattttagat 660
 |||||
 Sbjct: 768 ctagaattaatggagctgccctttgaattaagtaatttgaagcaagttacattttagat 827

Query: 661 atctcagcaacaagttttccagtggtcccaatctgtgtcctgcggatgtcgaatttgcag 720
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 Sbjct: 828 atctcagcaacaagttttccagtggtcccaatctgtgtcctgcggatgtcgaatttgcag 887

Query: 721 tggttggatatcagcagcaataacctgaccgacctgccgcaagatatagacaggctagag 780
 |||||
 Sbjct: 888 tggttggatatcagcagcaataacctgaccgacctgccgcaagatatagacaggctagag 947

Query: 781 gagctgcagagctttctctgtataaaaaacaagttgacctaccttcctattccatgctg 840
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 Sbjct: 948 gagctgcagagctttctctgtataaaaaacaagttgacctaccttcctattccatgctg 1007

Query: 841 aacctgaagaagctcactctgttagtcgtcagtggggaccatttgggtggagctcccaact 900
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 Sbjct: 1008 aacctgaagaagctcactctgttagtcgtcagtggggaccatttgggtggagctcccaact 1067

Query: 901 gccctttgtgactcatccacacctttaaaatttgtaagccttatggacaatcctattgat 960
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 Sbjct: 1068 gccctttgtgactcatccacacctttaaaatttgtaagccttatggacaatcctattgat 1127

Query: 961 aatgcccaatgtgaagatggcaatgaaataatggaaagtgaacgggatcgccaacatttt 1020
 |||||
 Sbjct: 1128 aatgcccaatgtgaagatggcaatgaaataatggaaagtgaacgggatcgccaacatttt 1187

Query: 1021 gataaagaagttatgaaagcctatattgaagaccttaagaaagagaatctgttcccagc 1080

Sbjct: 1188 |||||gataaagaagttatgaaagcctatattgaagaccttaaagaaagagaatctgttcccagc 1247

Query: 1081 tataaccaccaaagtgtcttttagccttcaactttga 1116

|||||
Sbjct: 1248 tataaccaccaaagtgtcttttagccttcaactttga 1283